SEQUENCE LISTING

GENERAL INFORMATION (1)

(i) APPLICANT:

> Seidel, Christoph; Weinhues, Ursula-Henrike; Schmitt, Urban; Motz, Manfred; Wiedmann, Michael; Upmeier, Barbara; Soutscheck, Erwin

(ii) TITLE OF INVENTION:

Recombinant antigen from the NS3 region of the hepatitis C virus

(iii) NUMBER OF SEQUENCES:

(iv) CORRESPONDENCE ADDRESS:

(A)

ADDRESSEE: Felfe & Lynch

(B) STREET: 805 Third Avenue

(C) CITY:

New York

(D) STATE:

New York

(E) COUNTRY: USA

(F) ZIP:

- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
 - (B) COMPUTER: IBM PS/2
 - (C) OPERATING SYSTEM: PC-DOS
 - SOFTWARE: PatentIn Relase #1.0, (D) Version #1.25 (EPA)
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/511,759
 - (B) FILING DATE: 7-AUGUST-1995y
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: p 44 28 705.4
 - (B) FILING DATE: 12 AUGUST 1994
- (viii) ATTORNEY/AGENT INFORMATION
 - (A) NAME: HANSON, NORMAN
 - (B) REGISTRATION NUMBER: 30, 946
 - (C) REFERENCE/DOCKET NUMBER: HUBR 1067.1
- (ix)TELECOMMUNICATION INFORMATION
 - (A) TELEPHONE: 212-688-9200
 - (B) TELEFAX: 212-838-3884

	(i)	() ()	3) I	ICE C LENGT TYPE: STRAN	H: nu IDEDN	885 clei ESS:	base c ac	pai id th	rs.							
	(ii) M	MOLECULE TYPE: cDNA													
	(vi	-	NITIA A) (AL OF ORGAN			atit	is C	C vir	rus						
	(vi	ii) POSITION IN GENOME: (A) CHROMOSOME SEGMENT: NS3														
Hong for the first first first from		()	HARA(A) 1 B) 1 EQUE1	NAME, LOCAT	KEY:	CDS	885	S	SEQ]	ID NO): 1:					
ATG Met																48
TTC	ACG Thr	GAT Asp	AAC Asn 20	TCC Ser	TCT Ser	CCA Pro	CCG Pro	GTA Val 25	GTG Val	CCC Pro	CAG Gln	AGC Ser	TTC Phe 30	CAG Gln	GTG Val	96
GCT Ala	CAC His	CTG Leu 35	His	GCT Ala	CCC Pro	ACA Thr	GGC Gly 40	AGC Ser	GGC Gly	AAG Lys	AGC Ser	ACC Thr 45	AAG Lys	GTC Val	CCG Pro	144
	Ala	Tyr	GCA Ala	Ala	Gln	Gly	Tyr	Lys		Leu	Val					192
GTT Val 65	Ala	GCA Ala	ACA Thr	TTG Leu	GGC Gly 70	TTT Phe	GGT Gly	GCC Ala	TAC Tyr	ATG Met 75	TCC Ser	AAG Lys	GCT Ala	CAT His	GGG Gly 80	240
ATC Ile	GAT Asp	CCT Pro	AAC Asn	ATC Ile 85	AGG Arg	ACC Thr	GGG Gly	GTG Val	AGA Arg 90	ACA Thr	ATT Ile	ACC Thr	ACT Thr	GGC Gly 95	AGC Ser	288
			TAC Tyr 100	Ser												336

1:

(2)

INFORMATION FOR SEQ ID NO:

			GCT Ala													384
			TCC Ser													432
ACT Thr 145	GCG Ala	GGG Gly	GCG Ala	AAA Lys	TTG Leu 150	GTT Val	GTG Val	TTC Phe	GCC Ala	ACC Thr 155	GCC Ala	ACC Thr	CCT Pro	CCG Pro	GGC Gly 160	480
TCC Ser	GTC Val	ACT Thr	GTG Val	CCC Pro 165	CAT His	CCC Pro	AAC Asn	ATT Ile	GAG Glu 170	GAG Glu	GTT Val	GCT Ala	CTA Leu	TCC Ser 175	ACC Thr	528
ACC Thr	GGA Gly	GAG Glu	ATC Ile 180	CCT Pro	TTT Phe	TAC Tyr	GGC Gly	AAG Lys 185	GCT Ala	ATC Ile	CCC Pro	CTT Leu	GAG Glu 190	GTA Val	ATC Ile	576
AAG Lys Q	GGG Gly	GGG Gly 195	AGA Arg	CAT His	CTC Leu	ATC Ile	TTC Phe 200	TGT Cys	CAT His	TCA Ser	AAG Lys	AGG Arg 205	AAG Lys	TGC Cys	GAT Asp	624
GAG GGlu	CTC Leu 210	GCC Ala	ACA Thr	AAG Lys	CTG Leu	GTC Val 215	GCA Ala	ATG Met	GGC Gly	ATC Ile	AAT Asn 220	GCC Ala	GTG Val	GCC Ala	TAC Tyr	672
TYT TYT 225	Arg	Gly	Leu	Asp	Val 230	Ser	Val	Ile	Pro	Thr 235	Ser	Gly	Asp	Val	Val 240	720
GTC Val	GTG Val	GCA Ala	ACC Thr	GAC Asp 245	GCC Ala	CTC Leu	ATG Met	ACC Thr	GGC Gly 250	TAT Tyr	ACC Thr	GGC Gly	GAC Asp	TTC Phe 255	GAC Asp	768
TCG	GTG Val	ATA Ile	GAC Asp 260	TGC Cys	AAC Asn	ACG Thr	TGT Cys	GTC Val 265	ACT Thr	CAG Gln	ACA Thr	GTC Val	GAT Asp 270	TTC Phe	AGC Ser	816
CTT Leu	GAC Asp	CCT Pro 275	ACC Thr	TTC Phe	ACC Thr	ATT Ile	GAG Glu 280	Thr	ACC Thr	ACA Thr	CTT Leu	CCC Pro 285	CAG Gln	GAT Asp	GCT Ala	864
			ACT Thr													885

(3) <u>INFORMATION FOR SEQ ID NO:</u> 2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 295 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Thr Met Ile Thr Asn Ser Arg Gly Ser Ile Met Lys Ser Pro Val 1 5 10 15

Phe Thr Asp Asn Ser Ser Pro Pro Val Val Pro Gln Ser Phe Gln Val 20 25 30

Ala His Leu His Ala Pro Thr Gly Ser Gly Lys Ser Thr Lys Val Pro 35 40 45

Ala Ala Tyr Ala Ala Gln Gly Tyr Lys Val Leu Val Leu Asn Pro Ser 55 60

Wal Ala Ala Thr Leu Gly Phe Gly Ala Tyr Met Ser Lys Ala His Gly
65 70 75 80

The Asp Pro Asn Ile Arg Thr Gly Val Arg Thr Ile Thr Thr Gly Ser

Pro Ile Thr Tyr Ser Thr Tyr Gly Lys Phe Leu Ala Asp Gly Gly Cys
100 105 110

Ala Gly Gly Ala Tyr Asp Ile Ile Ile Cys Asp Glu Cys His Ser Thr 115 120 125

Asp Ala Thr Ser Ile Leu Gly Ile Gly Thr Val Leu Asp Gln Gly Glu 130 135 140

Thr Ala Gly Ala Lys Leu Val Val Phe Ala Thr Ala Thr Pro Pro Gly 145 150 155 160

Ser Val Thr Val Pro His Pro Asn Ile Glu Glu Val Ala Leu Ser Thr 165 170 175

Thr Gly Glu Ile Pro Phe Tyr Gly Lys Ala Ile Pro Leu Glu Val Ile 180 185 190

Lys Gly Gly Arg His Leu Ile Phe Cys His Ser Lys Arg Lys Cys Asp 195 200 205

Glu	Leu 210	Ala	Thr	Lys	Leu	Val 215	Ala	Met	Gly	Ile	Asn 220	Ala	Val	Ala	Tyr
Tyr 225	Arg	Gly	Leu	Asp	Val 230	Ser	Val	Ile	Pro	Thr 235	Ser	Gly	Asp	Val	Val 240
Val	Val	Ala	Thr	Asp 245	Ala	Leu	Met	Thr	Gly 250	Tyr	Thr	Gly	Asp	Phe 255	Asp
Ser	Val	Ile	Asp 260	Cys	Asn	Thr	Cys	Val 265	Thr	Gln	Thr	Val	Asp 270	Phe	Ser
Leu	Asp	Pro 275	Thr	Phe	Thr	Ile	Glu 280	Thr	Thr	Thr	Leu	Pro 285	Gln	Asp	Ala
Val	Ser 290	Arg	Thr	Gln	Arg	Arg 295									

- INFORMATION FOR SEQ ID NO:
 - SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 40 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

AAGGGATCCA TCATGAAATC CCCGGTGTTC ACGGATAACT

(5) INFORMATION FOR SEQ ID NO:

- SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

GGGAAGCCTT AATTCTTACC GTCGTTGAGT GCGGGAGAC

	(6)	INFO	RMATION FOR SEQ ID NO: 5:	
		(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 39 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
		(ii)	MOLECULE TYPE: cDNA	
		(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 5:	
	GAGG	GATCC.	A TCATGAAAGC GGTGGACTTT ATCCCTGTG	39
	(7)	INFO	RMATION FOR SEQ ID NO: 6:	
from the form the fact that the fact that		(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 33 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
		(ii)	MOLECULE TYPE: cDNA	
The state of		(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 6:	
	GAGAA	AGCTT	TAACACGTGT TGCAGTCTAT CAC	33
The state of the s	(8)	INFO	RMATION FOR SEQ ID NO: 7:	
State of the state		(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 39 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
		(ii)	MOLECULE TYPE: cDNA	
		(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 7:	
~(\$*	GAGGG	ATCCA	A TCATGAAACA CCTGCATGCT CCCACCGGC	39

(8) INFORMATION FOR SEQ ID NO: (i) SEQUENCE CHARACTERISTICS: LENGTH: 33 base pairs (A) TYPE: nucleic acid (B) (C) STRANDEDNESS: single TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8: GAGAAGCTTT TAATACCAAG CACAGCCTGC GTC 33 (3) INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 302 amino acids (A) (B) TYPE: amino acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein The sourced (xi) SEQUENCE DESCRIPTION: Pro Val Glu Asn Leu Glu Thr Thr Met Arg Ser Pro Val Phe Thr Asp Asn Ser Ser Pro Pro Val Val Pro Gln Ser Phe Gln Val Ala His Leu His Ala Pro Thr Gly Ser Gly Lys Ser Thr Lys Val Pro Ala Ala Tyr Ala Ala Gln Gly Tyr Lys Val Leu Val Leu Asn Pro 55 Ser Val Ala Ala Thr Leu Gly Phe Gly Ala Tyr Met Ser Lys Ala His Gly Ile Asp Pro Asn Ile Arg Thr Gly Val Arg Thr Ile Thr Thr Gly Ser Pro Ile Thr Tyr Ser Thr Tyr Gly Lys Phe Leu Ala

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Asp	Gly	Gly	Cys	Ala 110	Gly	Gly	Ala	Tyr	Asp 115	Ile	Ile	Ile	Cys	Asp 120
Glu	Cys	His	Ser	Thr 125	Asp	Ala	Thr	Ser	Ile 130	Leu	Gly	Ile	Gly	Thr 135
Val	Leu	Asp	Gln	Gly 140	Glu	Thr	Ala	Gly	Ala 145	Lys	Leu	Val	Val	Phe 150
Ala	Thr	Ala	Thr	Pro 155	Pro	Gly	Ser	Val	Thr 160	Val	Pro	His	Pro	Asn 165
Ile	Glu	Glu	Val	Ala 170	Leu	Ser	Thr	Thr	Gly 175	Glu	Ile	Pro	Phe	Tyr 180
Gly	Lys	Ala	Ile	Pro 185	Leu	Glu	Val	Ile	Lys 190	Gly	Gly	Arg	His	Leu 195
Ile	Phe	Cys	His	Ser 200	Lys	Arg	Lys	Cys	Asp 205	Glu	Leu	Ala	Thr	Lys 210
Leu D	Val	Ala	Met	Gly 215	Ile	Asn	Ala	Val	Ala 220	Tyr	Tyr	Arg	Gly	Leu 225
Asp I	Val	Ser	Val	Tle 230	Pro	Thr	Ser	Gly	Asp 235	Val	Val	Val	Val	Ala 240
Thr				245					250					255
Ile I				260					265	•				270
Asp				275					280					285
Val	Ser	Arg	Thr	Gln 290	Arg	Arg	Gly	Arg	Thr 295	Gly	Arg	Gly	Lys	Pro 300
Gly	Ile													

Gly Ile 302

SEQUENCE PROTOCOL

- (1) GENERAL INFORMATION:
 - (i) APPLICANT:
 - (A) NAME: Boehringer Mannheim GmbH
 - (B) ROAD: Sandhofer Str. 112-132
 - (C) CITY: Mannheim
 - (E) COUNTRY: Germany
 - (F) POSTAL CODE: 68305
 - (ii) TITLE OF APPLICATION: Recombinant antigen from the NS3 region of the hepatitis C virus
 - (iii) NUMBER OF SEQUENCES: 8
 - (iv) COMPUTER READABLE FORM:
 - (A) DATA CARRIER: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPA)
- (2) INFORMATION FOR SEQ ID NO: 1:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 885 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRAND FORM: both
 - (D) TOPOLOGY: linear
 - (ii) TYPE OF MOLECULE: cDNA

(vi) INITIAL ORIGIN:

(A) ORGANISM: hepatitis C virus

(viii) POSITION IN THE GENOME:

(A) CHROMOSOME/SEGMENT: NS3

(ix) CHARACTERISTICS:

(A) NAME/KEY: CDS

(B) LOCATION: 1..885

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

	ACC Thr															48
TTC	ACG Thr															96
Company of the Compan	CAC His															144
	GCA Ala 50															192
GTT	GCT Ala															240
ATC	GAT	CCT	AAC	ATC	AGG	ACC	GGG	GTG	AGA	ACA	ATT	ACC	ACT	GGC	AGC	288
Ile	Asp	Pro	Asn	Ile 85	Arg	Thr	Gly	Val	Arg 90	Thr	Ile	Thr	Thr	Gly 95	Ser	
CCC Pro	ATT Ile	ACG Thr	TAC Tyr 100	TCC Ser	ACT Thr	TAC Tyr	GGC Gly	AAG Lys 105	TTT Phe	CTT Leu	GCC Ala	GAC Asp	GGC Gly 110	GGG Gly	TGC Cys	336
GCA Ala	GGG Gly	GGT Gly 115	GCT Ala	TAT Tyr	GAC Asp	ATA Ile	ATA Ile 120	ATT Ile	TGT Cys	GAC Asp	GAG Glu	TGC Cys 125	CAC His	TCC Ser	ACG Thr	384
GAT Asp	GCC Ala 130	ACA Thr	TCC Ser	ATC Ile	TTG Leu	GGC Gly 135	ATC Ile	GGC Gly	ACT Thr	GTC Val	CTT Leu 140	GAC Asp	CAA Gln	GGA Gly	GAG Glu	432

ACT Thr 145	GCG Ala	GGG Gly	GCG Ala	AAA Lys	TTG Leu 150	GTT Val	GTG Val	TTC Phe	GCC Ala	ACC Thr 155	GCC Ala	ACC Thr	CCT Pro	CCG Pro	GGC Gly 160	480
TCC Ser	GTC Val	ACT Thr	GTG Val	CCC Pro 165	CAT His	CCC Pro	AAC Asn	ATT Ile	GAG Glu 170	GAG Glu	GTT Val	GCT Ala	CTA Leu	TCC Ser 175	ACC Thr	528
						TAC Tyr										576
AAG Lys	GGG Gly	GGG Gly 195	AGA Arg	CAT His	CTC Leu	ATC Ile	TTC Phe 200	TGT Cys	CAT His	TCA Ser	AAG Lys	AGG Arg 205	AAG Lys	TGC Cys	GAT Asp	624
GAG Glu	CTC Leu 210	GCC Ala	ACA Thr	AAG Lys	CTG Leu	GTC Val 215	GCA Ala	ATG Met	GGC	ATC Ile	AAT Asn 220	GCC Ala	GTG Val	GCC Ala	TAC Tyr	672
						TCC Ser										720
Val Ū	GTG Val	GCA Ala	ACC Thr	GAC Asp 245	GCC Ala	CTC Leu	ATG Met	ACC Thr	GGC Gly 250	TAT Tyr	ACC Thr	GGC Gly	GAC Asp	TTC Phe 255	GAC Asp	768
TCG Ser	GTG Val	ATA Ile	GAC Asp 260	TGC Cys	AAC Asn	ACG Thr	TGT Cys	GTC Val 265	ACT Thr	CAG Gln	ACA Thr	GTC Val	GAT Asp 270	TTC Phe	AGC Ser	816
CTT Leu	GAC Asp	CCT Pro 275	ACC Thr	TTC Phe	ACC Thr	ATT Ile	GAG Glu 280	ACG Thr	ACC Thr	ACA Thr	CTT Leu	CCC Pro 285	CAG Gln	GAT Asp	GCT Ala	864
GEC Val	TCC Ser 290	CGC Arg	ACT Thr	CAA Gln	CGA Arg	CGG Arg 295										885

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 295 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) TYPE OF MOLECULE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

/207

Met Thr Met Ile Thr Asn Ser Arg Gly Ser Ile Met Lys Ser Pro Val

Phe Thr Asp Asn Ser Ser Pro Pro Val Val Pro Gln Ser Phe Gln Val Ala His Leu His Ala Pro Thr Gly Ser Gly Lys Ser Thr Lys Val Pro Ala Ala Tyr Ala Ala Gln Gly Tyr Lys Val Leu Val Leu Asn Pro Ser Val Ala Ala Thr Leu Gly Phe Gly Ala Tyr Met Ser Lys Ala His Gly Ile Asp Pro Asn Ile Arg Thr Gly Val Arg Thr Ile Thr Thr Gly Ser Pro Ile Thr Tyr Ser Thr Tyr Gly Lys Phe Leu Ala Asp Gly Gly Cys Ala Gly Gly Ala Tyr Asp Ile Ile Ile Cys Asp Glu Cys His Ser Thr Asp Ala Thr Ser Ile Leu Gly Ile Gly Thr Val Leu Asp Gln Gly Glu Thr Ala Gly Ala Lys Leu Val Val Phe Ala Thr Ala Thr Pro Pro Gly Ser Val Thr Val Pro His Pro Asn Ile Glu Glu Val Ala Leu Ser Thr 165 170 Thr Gly Glu Ile Pro Phe Tyr Gly Lys Ala Ile Pro Leu Glu Val Ile Lys Gly Gly Arg His Leu Ile Phe Cys His Ser Lys Arg Lys Cys Asp 200 Glu Leu Ala Thr Lys Leu Val Ala Met Gly Ile Asn Ala Val Ala Tyr 210 Tyr Arg Gly Leu Asp Val Ser Val Ile Pro Thr Ser Gly Asp Val Val Val Val Ala Thr Asp Ala Leu Met Thr Gly Tyr Thr Gly Asp Phe Asp Ser Val Ile Asp Cys Asn Thr Cys Val Thr Gln Thr Val Asp Phe Ser 260 Leu Asp Pro Thr Phe Thr Ile Glu Thr Thr Thr Leu Pro Gln Asp Ala 280 285

Val Ser Arg Thr Gln Arg Arg 290 295

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(2) INFORMATION FOR SEQ ID NO: 3:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 40 base pairs	
(B) TYPE: nucleic acid	
(C) STRAND FORM: single	
(D) TOPOLOGY: linear	
(ii) TYPE OF MOLECULE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:	
AAGGGATCCA TCATGAAATC CCCGGTGTTC ACGGATAACT	40
(2) INFORMATION FOR SEQ ID NO: 4:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 39 base pairs	
(B) TYPE: nucleic acid	
(C) STRAND FORM: single	
(D) TOPOLOGY: linear	
(ii) TYPE OF MOLECULE: CDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4	
GGGAAGCCTT AATTCTTACC GTCGTTGAGT GCGGGAGAC	39
(2) INFORMATION FOR SEQ ID NO: 5:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 39 base pairs	
(B) TYPE: nucleic acid	
(C) STRAND FORM: single	

(ii) TYPE OF MOLECULE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5	
GAGGGATCCA TCATGAAAGC GGTGGACTTT ATCCCTGTG	39
(2) INFORMATION FOR SEQ ID NO: 6:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 33 base pairs	
(B) TYPE: nucleic acid	
(C) STRAND FORM: single	
(D) TOPOLOGY: linear	
(ii) TYPE OF MOLECULE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6	
GAGAAGCTTT TAACACGTGT TGCAGTCTAT CAC	33
(2) INFORMATION FOR SEQ ID NO: 7:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 39 base pairs	
(B) TYPE: nucleic acid	
(C) STRAND FORM: single	
(D) TOPOLOGY: linear	
(ii) TYPE OF MOLECULE, COM	

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:	
GAGGGATCCA TCATGAAACA CCTGCATGCT CCCACCGGC	39
(2) INFORMATION FOR SEQ ID NO: 8:	•
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 33 base pairs	
(B) TYPE: nucleic acid	
(C) STRAND FORM: single	
(D) TOPOLOGY: linear	
(ii) TYPE OF MOLECULE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8	
GAGAAGCTTT TAATACCAAG CACAGCCTGC GTC	33